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=> d his

     (FILE 'HOME' ENTERED AT 08:30:58 ON 18 DEC 2003)

     FILE 'DISSABS, 1MOBILITY, AGRICOLA, AQUASCI, BIOTECHNO, COMPENDEX,
     COMPUAB, CONF, CONFSCI, ELCOM, HEALSAFE, IMSDRUGCONF, LIFESCI, OCEAN,
     MEDICONF, PASCAL, PAPERCHEM2, POLLUAB, SOLIDSTATE, ADISCTI, ADISINSIGHT,
     ADISNEWS, ANABSTR, BIOBUSINESS, BIOCOMMERCE, ...' ENTERED AT 08:31:33 ON
     18 DEC 2003
                 E MAYO STEPHEN?/AU
L1            11 S E1 OR E2 OR E4
                 E SHIFMAN JULIA?/AU
L2            16 S E1 OR E2 OR E4
                 E SHIMAOKA MOTOMU?/AU
L3            84 S E1 OR E2
                 E SPRINGER TIMOTHY?/AU
                 E SPRINGER?/AU
L4          1827 S ((BIASED OR OPEN OR CLOSE OR CONFORMATION)(S) (I (A) DOMAIN))
L5            30 S L4 AND(L1 OR L2 OR L3)
L6            13 DUP REM L5 (17 DUPLICATES REMOVED)
L7            77 S L4 (S) (ALPHA (A) M)
L8            14 S L7 (S) (139 OR 153 OR 156 OR 157 OR 160 OR 199 OR 215 OR 21
L9            11 DUP REM L8 (3 DUPLICATES REMOVED)

     FILE 'DISSABS, 1MOBILITY, AGRICOLA, AQUASCI, BIOTECHNO, COMPENDEX,
     COMPUAB, CONF, CONFSCI, ELCOM, HEALSAFE, IMSDRUGCONF, LIFESCI, OCEAN,
     MEDICONF, PASCAL, PAPERCHEM2, POLLUAB, SOLIDSTATE, ADISCTI, ADISINSIGHT,
     ADISNEWS, ANABSTR, BIOBUSINESS, BIOCOMMERCE, ...' ENTERED AT 08:55:30 ON
     18 DEC 2003

     FILE 'DISSABS, 1MOBILITY, AGRICOLA, AQUASCI, BIOTECHNO, COMPENDEX,
     COMPUAB, CONF, CONFSCI, ELCOM, HEALSAFE, IMSDRUGCONF, LIFESCI, OCEAN,
     MEDICONF, PASCAL, PAPERCHEM2, POLLUAB, SOLIDSTATE, ADISCTI, ADISINSIGHT,
     ADISNEWS, ANABSTR, BIOBUSINESS, BIOCOMMERCE, ...' ENTERED AT 08:56:58 ON
     18 DEC 2003
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L6 ANSWER 13 OF 13 BIOSIS COPYRIGHT 2003 BIOLOGICAL ABSTRACTS INC. on STN
DUPLICATE 11

ACCESSION NUMBER: 2000:451152 BIOSIS
DOCUMENT NUMBER: PREV200000451152
TITLE: Computational design of an integrin **I domain** stabilized in the **open** high affinity **conformation**.
AUTHOR(S): **Shimaoka, Motomu**; **Shifman, Julia M.**; Jing, Hua; Takagi, Junichi; Mayo, Stephen L. [Reprint author]; Springer, Timothy A.
CORPORATE SOURCE: Howard Hughes Medical Institute and Division of Biology, California Institute of Technology, mail-code 147-75, Pasadena, CA, 91125, USA
SOURCE: Nature Structural Biology, (August, 2000) Vol. 7, No. 8, pp. 674-678. print.
ISSN: 1072-8368.
DOCUMENT TYPE: Article
LANGUAGE: English
ENTRY DATE: Entered STN: 25 Oct 2000
Last Updated on STN: 10 Jan 2002

AB We have taken a computational approach to design mutations that stabilize a large protein domain of apprx200 residues in two alternative conformations. Mutations in the hydrophobic core of the alphaMbeta2 integrin **I domain** were designed to stabilize the crystallographically defined **open** or closed conformers. When expressed on the cell surface as part of the intact heterodimeric receptor, binding of the designed **open** and closed **I domains** to the ligand iC3b, a form of the complement component C3, was either increased or decreased, respectively, compared to wild type. Moreover, when expressed in isolation from other integrin domains using an artificial transmembrane domain, designed **open I domains** were active in ligand binding, whereas designed closed and wild type **I domains** were inactive. Comparison to a human expert designed open mutant showed that the computationally designed mutants are far more active. Thus, computational design can be used to stabilize a molecule in a desired **conformation**, and conformational change in the **I domain** is physiologically relevant to regulation of ligand binding.